



FIG. 1A

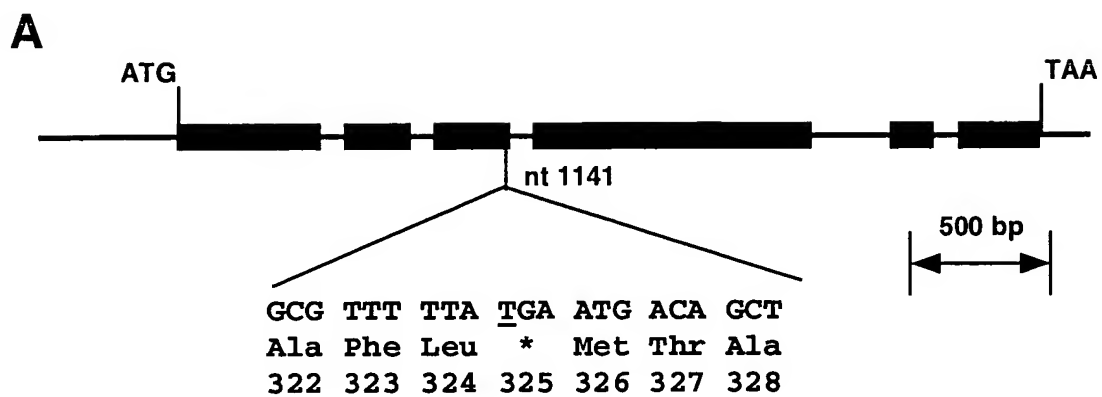


FIG. 1B

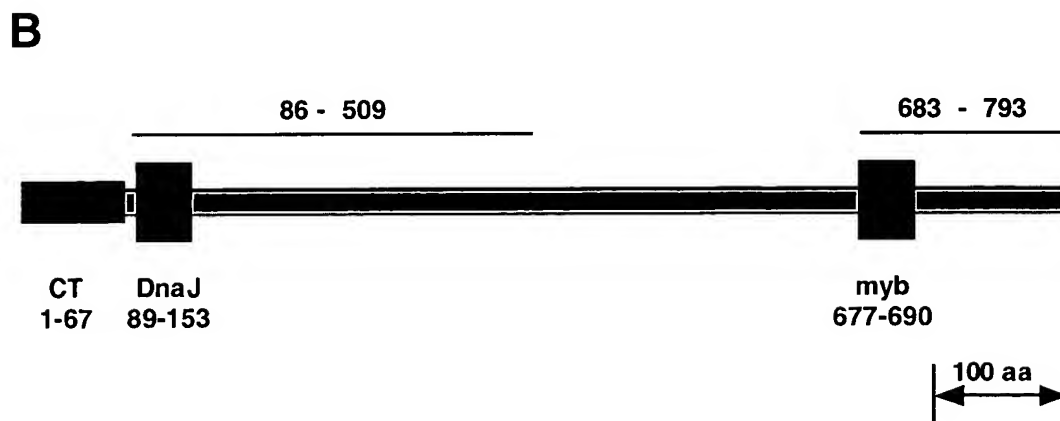


FIG. 2

Q9SAG8/55-115	DEYKTLKURPD	SSYE	VKA	FR	LAK	KY	HPD	VCR	GSN	QFOT	NE	AV	DI	VL	KQ	IK	QME	----	
P93499/67-134	SLYDILGIPAG	ASSQE	IKAA	VR	RLAR	VCH	PD	VA	ID	FMK	HA	AV	ST	SPP	DK	RAN	YD	----	
O48828/68-135	SLYEILETPVG	STSQE	IKSA	VR	RLAR	ICH	PD	VAR	NS	FMK	HA	AV	CT	SDP	EX	RA	VD	----	
DNJL_MYCPN/2-64	TYDILELPQT	ATLOE	IKTA	YK	LAK	KRY	HPD	INK	Q	FKV	KN	AV	AV	LS	TQ	KA	EYD	----	
DNJL_MYCGE/2-64	NYDILLELPTT	ASIKE	IKIA	YK	LAK	KRY	HPD	VNK	L	FVE	IN	NA	YS	IL	SDP	NO	KE	----	
Q9SDN0/66-133	SYDILGVTES	VTLPE	IKQAY	KOL	ARK	KY	HPD	VSP	PD	FIR	Q	E	AY	ET	SDP	RR	VL	----	
Q9VXT2/31-99	NCYDVLGVIRE	SSKSE	IGKAY	Q	LARR	YHPD	LHR	GA	----	FKL	VAT	AY	ET	LR	EE	ES	RT	----	
Q17433/36-105	NCYDVLGVANREE	FDKQK	LAKAY	RL	ARK	KY	HPD	VKN	K	FRV	TAT	AV	ET	LK	DD	EAK	T	----	
Q9SH08/76-147	SPYDTLELDRN	AEEEQ	IKVAV	RL	LAK	KY	HPD	VYD	KG	FIK	QA	AY	ET	LK	DD	EAK	T	----	
O94657/6-73	KNDILEVHFE	ASAE	IKKS	YK	RL	ALL	HPD	KA	PIH	FRG	Q	E	AY	DI	LK	PD	ES	----	
*maize	DEYKULGAEP	HFLGD	GIRRA	FES	IR	AK	PPQ	YGS	TEAL	AG	RQ	----	MLQ	IA	HD	T	NO	----	
*rice/97-162	DEYKVLGAEP	HFLGD	GIRRA	FES	IR	AK	PPQ	YGS	TEAL	AG	RQ	----	MLQ	IA	HD	T	NO	----	
*potato/109-174	DEYRVLGAEA	HFLGD	GIRRC	YDAR	ITK	PPQ	YGS	Q	EAL	IG	RQ	----	ILQ	AA	CET	L	ADS	----	
*Mtrunc/	DIYKULGAET	HFLGD	GIRRA	YEA	K	FSK	PPQ	YAFS	NEAL	IS	RQ	----	ILQ	AA	CET	L	ADS	----	
*Athal/89-154	DEYQVLGAQT	HFLTD	GIRRA	FES	IR	AK	PPQ	YGS	TEAL	AG	RQ	----	MLQ	IA	HD	T	NO	----	
*Pm_MED4/6-71	DHFRLLGVSP	SATSE	EILRA	FQ	LR	LDK	TP	DE	GFT	YEV	L	TQ	SE	----	LI	RL	TAD	----	
*Pm_MIT9313/11-76	DHFRLLGVSP	SADSE	ALRA	LE	LR	LDK	TP	DE	GFT	YEV	L	TQ	SE	----	LI	RL	TAD	----	
*ScC_WH8102/6-71	DHFRLLGVSP	SADPA	SILRL	Q	TR	SDS	PPD	CG	FT	HEG	L	L	Q	RA	----	LI	RL	TAD	----
*Syn_PCC6803/6-71	DHFRLLGVSP	QSGGE	TIEQAY	Q	DR	LLQ	L	PR	RE	FS	DA	AV	T	LR	NO	----	LI	RL	----
*Nostoc/6-71	DYRVLGLPL	AASEE	QLRAY	SDR	IVQ	L	PR	RE	YS	QAA	IS	RQ	----	LI	EEAY	V	LS	----	
*Anabena/16-81	DYRVLGLPL	AASDE	QLRAY	SDR	IVQ	L	PR	RE	YS	QAA	IS	RQ	----	LI	EEAY	V	LS	----	
Q9U6V7/17-82	DYVALLGCD	NSTVE	QITAEY	KIL	ALQ	HH	PD	KND	G	EKEA	EM	KFQ	----	LI	KEA	KE	L	----	
Q9TVP3/17-82	DFYGLHCDE	NSSPE	QIQAEY	KVL	ALQ	HH	PD	KNS	G	DKEA	EAK	FQ	----	LI	KEA	KE	L	----	
Q9R022/14-79	DYVALLGCD	LSSVE	QILAEF	KIL	ALQ	HH	PD	KHP	E	NSK	AV	ET	FQ	----	LI	KEA	KE	----	
Q9VN28/708-772	DAYSTLGVPP	DSSQE	QIRKHY	KK	TAV	L	HPD	KNK	----	QAGA	E	EAFK	----	LI	Q	RA	FEL	----	
O97211/9-72	ELAYQVELDA	QCTTA	ETISQY	RR	L	ALR	YHPD	RN	AG	----	AT	VEO	FQ	----	LI	EEA	H	----	
O13601/12-78	DYVALLGAE	TSSYV	EIRQY	K	L	VR	YHPD	RN	GRE	A	EVL	PO	FQ	----	LI	Q	RA	----	
O94566/12-78	DYVALKLQK	NATFQ	QIRKQ	L	FL	ALQ	YHPD	RN	PD	DE	E	AVK	RQ	----	LI	Q	RA	----	
Q9UUG3/2-69	NEYSVLNKDGK	TYTDD	EIKEAY	R	K	ALL	FHPD	KCK	----	EKPS	V	VYT	TDQ	----	LI	KEA	Q	----	

FIG. 3B

[illegible]

Human_Dynamin-1	1	-----MGNRQMEDLIPLVNRLODAPS-----AIGQNADLDLPQIAVVGQSAGKESVLENFVGR
Yeast_Dnm1p	1	-----MAS--LMDLIPTVNRKLDVMY-----DSGIDT-LDLPILAVGQS88GKESILNLTIVGR
ARC5	1	MAEVSAKSVTVENAEEDDAAIERNSLYEAYNELHALAOELETTPPEAPVAVVGQQTDDGSAIVKALMGF
Human_Dynamin-1	64	VERRPLVQLVNAAT-----EYABEPLHCKOKKET
Yeast_Dnm1p	61	VERRPLVQLVNAAT-----EYABEPLHCKOKKET
ARC5	81	KERRPLTHMKYDPCQPP-----LCHLGSDDDDPSVSLPK
Human_Dynamin-1	102	EARTDEVGT-NKGISPVPEENRNVYSPHVMELVLDLGMTKRVVGQD--PPDIEFQIRDMEMQFVTKBNC
Yeast_Dnm1p	141	ENETATIAQK-DKGISKIPENRNVYSPHVMELVLDLGMTKRVVGQD--PPDIEFQIRDMEMQFVTKBNC
ARC5	125	EARNMELEQBPCSEPPSAKEHIVKQYKPCPMLTIDTGLIAPAPQKLNALQVQARAVEALVRAKMQHKB
Human_Dynamin-1	179	QDLANSDAIKVAKVEPQGOQKMGVIAKQDUMDEGTDAKDVLNKLLEPRRGYIGVNVRSQKDDIGKEDIT
Yeast_Dnm1p	218	VLVNSESILKARVDDQGRKRGVIRKGGDMDSGENALDILSGKMYELKLGEGVGVNRSQKDDIQLNETVE
ARC5	205	GDWSIATTRFVMDQDELSRGLVMSKEDTKIPQFSCSSDVEVFLSEP-----ASALDSSLGDSPPP
Human_Dynamin-1	259	FLSHPSYRHLADRMGTPYVQKVINQQLINHIRDTLPGLRNKLOQLLSRKBYBXYKNRPDDPARKTKAL
Yeast_Dnm1p	298	FRKHEVNRATLSTKCGTRYELAKLNQTLSSHIRDKLPDDIKTKLNELISQTEQLARXGCVGATTNESRSLV
ARC5	278	YQDSVYKNSNDEPKQAVSIREMEDIASLEKELGRLTKQBSKSHIGISKRLPLFEBLLYKRYKESVPLIIP
Human_Dynamin-1	339	DEERAKSCGQDQIDTYEESC-GARINRLEHERPPPELVMEPPDERELRREISYAIKENHIGIRIGITPDMA
Yeast_Dnm1p	378	NEISSIDGSSDINTRELCO-GARLYIYNNVGN8KESIDPTSNLSVLDVRIARNSTGPRPTLEVPBET
ARC5	358	RKLDVSKELSSLDBAKBERQRTPHDLGLTKLSLLKGTVPAPDPRPGETLQDERTQCGAPV@TDGLQPG
Human_Dynamin-1	418	KKTRHPCLKQVDMVISEL-----STVRQC-TKKLQVPRLEEMERIYTHIREREGRTKEQVM
Yeast_Dnm1p	457	KLLLEPSQRCVRLVYBELM-----KICHKCGSABEAPRKLSMELVISELIRERLQPTRSYVE
ARC5	438	RLYGAQYHRAMAEERELVGAIKCPPIITREIEVNAQGVEDHDTGNTYSRTACVIAVAKARETFEFLHQLG
Human_Dynamin-1	486	ENTNHEDELOFANAQQRSNQMNKKTSGNQDBILVIRKGMWITINNIGIMKQOSEBYWFLTAENLSWYKDD
Yeast_Dnm1p	526	ENTNHEPNEL--SATEAMDDIMKTRKRNQ--LLESKLSQBNQGTNGING-----TSSISNIDQD
ARC5	518	ULPISVYLQKBGBYLSQHEVPLEKVASAFNPFVSTESKCRDKCHEDTASTR-----YVTWSLHNKN
Human_Dynamin-1	566	SVDNKLRDVERGFMSSKHIFALPN-EEQRNVYKDYRQLELACETQEEVDSWKASELRAGVYPERVGDKEK
Yeast_Dnm1p	593	DGIDAKSKQTKDKLN--YFEGKDK-KQQVPDASDEKRSINQD-----GNIBDERNLQSDPSLGDIDD
ARC5	591	SPGCTEHTTSGNATGFSLPQDALGCTDTRSRSDVKLSHESNIDSGSSIQTTEMRLADLDSLWNREL
Human_Dynamin-1	645	DSPMHSMDPQLERQVETIRNLVDSXMAIVNKTMRDLMPTETIHLMDNNTREPIFSELLANEYSQGDQNTEN
Yeast_Dnm1p	661	-----PETERBELSCPLERKRLVSVPDIREMDEDOVPRAYMCLIVNYCDSVQNRRLVTKRYKETLPBELL
ARC5	668	-----IVYALVQDPPQGEREVELASAEKLFNCPLELMPIVDKPALREBEENAPEDDDLSIFDITNER
Human_Dynamin-1	725	RDEMLRMYHALKEALSTIGNINTITVSTPMPEPPVDDSWLQVQSVAPAGRRSPTSSPTPQRRAPAVPPARPQS
Yeast_Dnm1p	736	RELCKVKSQGVYKKAATLISNII-----
ARC5	740	TEBELRVRKREKPRVNEKLNSEPAQN-----LKAPSVOH-----
Human_Dynamin-1	805	AGSALGGAPPVPSRPGASDPDPGPPPPQVPSRPNRAPPGVPSRSGQASPSRPPPPDL
Yeast_Dnm1p		-----
ARC5		-----

FIG. 4